GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 09:31:24 ; Search time 158 Seconds
(without alignments)
6352.565 Million cell updates/sec

Title: US-09-494-297-1
Perfect score: 2274
Sequence: 1 atgaaaaaaacaaggtttcc.....ggataagaaaacatgactag 2274

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	53.4	2.3	7218	1	US-08-232-463-14	Sequence 14, Appl
c	2	50.2	2.2	15016	4	US-09-601-198-60	Sequence 60, Appl
	3	49.6	2.2	3095	6	5231168-1	Patent No. 5231168
	4	48.2	2.1	876	3	US-08-446-137B-3	Sequence 3, Appli
	5	48.2	2.1	3279	3	US-08-446-137B-1	Sequence 1, Appli
	6	48.2	2.1	20674	4	US-09-641-638-651	Sequence 651, App
	7	47.4	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	8	47	2.1	1785	4	US-09-601-198-156	Sequence 156, App
c	9	47	2.1	2418	4	US-09-601-198-61	Sequence 61, Appl
c	10	46.8	2.1	5340	4	US-09-627-122-21	Sequence 21, Appl
c	11	46.8	2.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	12	46.6	2.0	10640	4	US-09-417-485D-5	Sequence 5, Appli
	13	46.4	2.0	5361	3	US-08-973-462-2	Sequence 2, Appli
	14	46.4	2.0	6152	3	US-08-973-462-1	Sequence 1, Appli
	15	45.4	2.0	1380	4	US-09-491-785-1	Sequence 1, Appli
c	16	44.8	2.0	3308	3	US-08-714-918-68	Sequence 68, Appl
c	17	44.8	2.0	3308	3	US-09-265-315-68	Sequence 68, Appl
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c	19	44.8	2.0	3308	3	US-09-266-417-68	Sequence 68, Appl
	20	44.6	2.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	21	44.4	2.0	5652	4	US-09-601-198-75	Sequence 75, Appl
c	22	44.4	2.0	14066	4	US-09-601-198-56	Sequence 56, Appl
c	23	43.4	1.9	732	4	US-09-601-198-112	Sequence 112, App
	24	43.4	1.9	1149	4	US-09-601-198-151	Sequence 151, App
c	25	43.2	1.9	20674	4	US-09-641-638-651	Sequence 651, App
	26	43	1.9	1329	4	US-09-134-001C-196	Sequence 196, App
	27	42.8	1.9	1107	4	US-09-134-001C-1072	Sequence 1072, Ap
	28	42.4	1.9	429	1	US-07-710-361-6	Sequence 6, Appli
	29	42.4	1.9	943	4	US-09-071-035-179	Sequence 179, App
	30	42.4	1.9	1023	4	US-09-071-035-177	Sequence 177, App
	31	42.4	1.9	1055	1	US-08-702-344-18	Sequence 18, Appl
	32	42.4	1.9	1405	1	US-07-710-361-3	Sequence 3, Appli
	33	42.4	1.9	1956	4	US-08-559-896B-1	Sequence 1, Appli
	34	42.4	1.9	2210	1	US-07-710-361-2	Sequence 2, Appli
	35	42	1.8	2043	4	US-09-601-198-181	Sequence 181, App
c	36	41.8	1.8	636	4	US-09-601-198-12	Sequence 12, Appl
c	37	41.8	1.8	1374	4	US-09-601-198-131	Sequence 131, App
	38	41.8	1.8	4507	2	US-08-568-459A-3	Sequence 3, Appli
	39	41.8	1.8	4507	2	US-08-487-826B-3	Sequence 3, Appli
	40	41.8	1.8	4507	4	US-09-210-288-3	Sequence 3, Appli
	41	41.8	1.8	11091	4	US-09-134-001C-2243	Sequence 2243, Ap
	42	41.6	1.8	2223	1	US-08-257-073-4	Sequence 4, Appli
c	43	41.6	1.8	3396	4	US-09-601-198-74	Sequence 74, Appl
	44	41.4	1.8	747	4	US-09-328-352-876	Sequence 876, App
c	45	41.4	1.8	2814	1	US-07-781-034-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match 2.3%;  Score 53.4;  DB 1;  Length 7218;
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Best Local Similarity 9.3%; Pred. No. 0.003;
Matches 42; Conservative 215; Mismatches 196; Indels 0; Gaps 0;

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Db       1463 GTAGTTAAAGAGATAGAAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1404

Qy       1840 GGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAAATAATAAG 1899
Db       1403 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1344

Qy       1900 CAAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAACCTCGAATTTAAAGATGGT 1959
Db       1343 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1284

Qy       1960 AAAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGT 2019
Db       1283 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1224

Qy       2020 TATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGCCAA 2079
Db       1223 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1164

Qy       2080 GAAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTT 2139
Db       1163 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1104

Qy       2140 GAAAATAATAAAGAGCCTGTTGTTCCTACAGGAGTTGATCAAAAGATCAATGGCTATCTA 2199
Db       1103 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCA 1044

Qy       2200 GCTTTGATAGTTATCGCTGGTATCAGTTTGGGG 2232
Db       1043 GCCAAGCTCGGAATTAATTCTGTGAGCGTATGG 1011
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RESULT 2
US-09-601-198-60/c
; Sequence 60, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellson Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15016
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-60

Query Match 2.2%; Score 50.2; DB 4; Length 15016;
Best Local Similarity 47.5%; Pred. No. 0.021;
Matches 182; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

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Qy       1781 AAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAACGGTGACTG 1840
Db       7274 ATGTTAAATATGCTTTATTTAATCAAACGCAAAATGCTAATTTAATTAACAATATTACAA 7215

Qy       1841 GTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAAATAATAAGC 1900
Db       7214 TTAAATATGATCAACAAAATAAACAATTCTATTGTGAATTTGATATTGATAATTTAACTT 7155

Qy       1901 AAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAACCTCGAATTTAAAGATGGTA 1960
Db       7154 TAAATCAAGATTATGGTATTTTTGAAATTAGTTTTGCTAATAAACCAATTCATGCCGCAT 7095

Qy       1961 AAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTT 2020
Db       7094 TTGCTAAAATTAATGATACCCA---ACATCCTTTAGCTCTTTTAAGTACTAATAATCAAG 7038

Qy       2021 ATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGCCAAG 2080
Db       7037 ATATAAATCAAAAAATTGCTTTAGATTGTGAAGTTAATAAAGTTACAATTAATAAACAAG 6978

Qy       2081 AAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTG 2140
Db       6977 ATCTTGATTATGATCAAAACACCAAGATTAGTTGACCGATTGAATTAAGTTCTAATTTAT 6918

Qy       2141 AAAATAATAAAGAGCCTGTTGTT 2163
Db       6917 TAAACAATAAGTACATTCGTGTT 6895
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RESULT 3
5231168-1
;Patent No. 5231168
; APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
; TITLE OF INVENTION: MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/409,658
; FILING DATE: 18-SEP-1989
;SEQ ID NO:1:
; LENGTH: 3095
5231168-1

Query Match 2.2%; Score 49.6; DB 6; Length 3095;
Best Local Similarity 42.4%; Pred. No. 0.018;
Matches 268; Conservative 0; Mismatches 364; Indels 0; Gaps 0;

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Qy       1513 ACACAATTGCGTGCGGCTACTCAGTTAGCAATATATTATTTCACTGATAGTGCTGAATTA 1572
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Db       1537 AAAGTTCAACATGAAATAGTAGAAGTTGAAGAAATTCTACCAGAAGATAAAAATGAAAAA 1596

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Qy       2053 GGCTATAAGGTTAAAGTTAATAGCCAAGAAGT 2084

Db       1657 GGTCAACATGAAATAGTAGAGGTTGAAGAAAT 1688


RESULT 4
US-08-446-137B-3
; Sequence 3, Application US/08446137B
; Patent No. 6162903
;  GENERAL INFORMATION:
;    APPLICANT:  Trowern, Angus R.
;    APPLICANT:  Atkinson, Anthony
;    APPLICANT:  Murphy, Jonathan P.
;    APPLICANT:  Laurence, Oliver S.
;    APPLICANT:  Duggleby, Clive J.
;    TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEINS DERIVED
;    TITLE OF INVENTION:  FROM L PROTEIN AND THEIR USES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,137B
;      FILING DATE:  22-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  100084.406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Peptostreptococcus
;      STRAIN:  1018
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..876
US-08-446-137B-3

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  Best Local Similarity   46.7%;  Pred. No. 0.026;
  Matches  189;  Conservative    0;  Mismatches  213;  Indels    3;  Gaps    1;

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Qy       1421 ATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGG 1465

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RESULT 5
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; Sequence 1, Application US/08446137B
; Patent No. 6162903
;  GENERAL INFORMATION:
;    APPLICANT:  Trowern, Angus R.
;    APPLICANT:  Atkinson, Anthony
;    APPLICANT:  Murphy, Jonathan P.
;    APPLICANT:  Laurence, Oliver S.
;    APPLICANT:  Duggleby, Clive J.
;    TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEINS DERIVED
;    TITLE OF INVENTION:  FROM L PROTEIN AND THEIR USES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,137B
;      FILING DATE:  22-MAY-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  100084.406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3279 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
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;      ORGANISM:  Peptostreptococcus asaccharolyticus
;      STRAIN:  1018
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  103..3186
;      IDENTIFICATION METHOD:  experimental
;      OTHER INFORMATION:  /codon_start= 280
;      OTHER INFORMATION:  /product= "mature protein L"
;      OTHER INFORMATION:  /evidence= EXPERIMENTAL
;      OTHER INFORMATION:  /number= 1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  103..3186
;      OTHER INFORMATION:  /codon_start= 103
;      OTHER INFORMATION:  /product= "immature protein L"
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  280..3183
;      OTHER INFORMATION:  /codon_start= 280
;      OTHER INFORMATION:  /product= "mature protein L"
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;      NAME/KEY:  misc_signal
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US-08-446-137B-1

  Query Match             2.1%;  Score 48.2;  DB 3;  Length 3279;
  Best Local Similarity   46.7%;  Pred. No. 0.039;
  Matches  189;  Conservative    0;  Mismatches  213;  Indels    3;  Gaps    1;

Qy       1061 ATAGTATCGCAGAGCCAATCACTTTTAAGGTTGAAGCTGGCAAAGTGTATACTATTATTG 1120
              | | |  || | |  ||      ||  | | ||  |    || | |  | | ||   |||
Db       1310 AAAATGGCGAATATACAGCAGACTTAGAAGATGGTGGAAACACAATCAACATTAAATTTG 1369

Qy       1121 ATGGAAAACAGATTGAAAATCCCAATAAAGAGATAGTAGAGCCTTACTCAGTAGAAGCAT 1180
               ||||||| | |    | |  |     ||||   |  |||         || |  |||
Db       1370 CTGGAAAAGAAACACCAGAAACACCAGAAGAACCAAAAGAAGAAGTTACAATCAAAGTTA 1429

Qy       1181 ATAATGATTTTGAAGAATTTAGCGTTTTAACTACACAAAACTATGCAAAATTTTATTATG 1240
              |       |||| |||    |   |   |||  || ||  | | | || |||| |  | |
Db       1430 ACTTAATCTTTGCAGATGGAAAGATACAAACAGCAGAATTCAAAGGAACATTTGAAGAAG 1489

Qy       1241 CAAAAAATAAAAATGGAAGTTCACAGGTTGTCTATTGCTTTAATGCAGATCTAAAATCTC 1300
              ||| |     ||| |    | |  | |    ||  |     || | | ||    ||| |
Db       1490 CAACA---GCAAAAGCTTATGCTTATGCAAACTTATTAGCAAAAGAAAATGGCGAATATA 1546

Qy       1301 CACCAGACTCTGAAGATGGTGGGAAAACAATGACTCCAGACTTTACAACAGGAGAAGTAA 1360
              || ||||||  |||||||||||| || ||||| |      | ||| |   |  ||||  |
Db       1547 CAGCAGACTTAGAAGATGGTGGAAACACAATCAACATTAAATTTGCTGGAAAAGAAACAC 1606

Qy       1361 AATACACTCATATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGAGATACCG 1420
               | | || |     | |      ||     ||| |   |  || ||   ||    | | |
Db       1607 CAGAAACACCAGAAGAACCAAAAGAAGAAGTTACAATCAAAGTTAACTTAATCTTTGCAG 1666

Qy       1421 ATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGG 1465
              ||    | ||      |  | |  ||||  |  | ||||  | |
Db       1667 ATGGAAAAACACAAACAGCAGAATTCAAAGGAACATTTGAAGAAG 1711


RESULT 6
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
;  TITLE OF INVENTION:  GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
;  FILE REFERENCE:  GENSET.051CP1
;  CURRENT APPLICATION NUMBER: US/09/641,638
;  CURRENT FILING DATE:  2000-08-16
;  PRIOR APPLICATION NUMBER:  US 09/502,330
;  PRIOR FILING DATE:  2000-02-11
;  PRIOR APPLICATION NUMBER:  US 60/133,200
;  PRIOR FILING DATE:  1999-05-07
;  PRIOR APPLICATION NUMBER:  US 09/275,267
;  PRIOR FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER:  US 60/119,917
;  PRIOR FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS:  1304
;  SOFTWARE:  Patent.pm
; SEQ ID NO 651
;  LENGTH: 20674
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 1123..3123
;  OTHER INFORMATION: 5'regulatory region
;  NAME/KEY: exon
;  LOCATION: 3124..3297
;  OTHER INFORMATION: exon 1
;  NAME/KEY: exon
;  LOCATION: 3871..4072
;  OTHER INFORMATION: exon 2
;  NAME/KEY: exon
;  LOCATION: 5552..5633
;  OTHER INFORMATION: exon 3
;  NAME/KEY: exon
;  LOCATION: 5758..5880
;  OTHER INFORMATION: exon 4
;  NAME/KEY: exon
;  LOCATION: 5996..6099
;  OTHER INFORMATION: exon 5
;  NAME/KEY: exon
;  LOCATION: 6349..6509
;  OTHER INFORMATION: exon 6
;  NAME/KEY: exon
;  LOCATION: 7379..7522
;  OTHER INFORMATION: exon 7
;  NAME/KEY: exon
;  LOCATION: 8645..8854
;  OTHER INFORMATION: exon 8
;  NAME/KEY: exon
;  LOCATION: 12254..12340
;  OTHER INFORMATION: exon 9
;  NAME/KEY: exon
;  LOCATION: 12854..13023
;  OTHER INFORMATION: exon 10
;  NAME/KEY: exon
;  LOCATION: 13308..13429
;  OTHER INFORMATION: exon 11
;  NAME/KEY: exon
;  LOCATION: 16567..16667
;  OTHER INFORMATION: exon 12
;  NAME/KEY: exon
;  LOCATION: 16775..16945
;  OTHER INFORMATION: exon 13
;  NAME/KEY: exon
;  LOCATION: 17063..17554
;  OTHER INFORMATION: exon 14
;  NAME/KEY: misc_feature
;  LOCATION: 17555..20674
;  OTHER INFORMATION: 3'regulatory region
;  NAME/KEY: allele
;  LOCATION: 1128
;  OTHER INFORMATION: 10-508-191  : polymorphic base C or T
;  NAME/KEY: allele
;  LOCATION: 1182
;  OTHER INFORMATION: 10-508-245  : polymorphic base C or T
;  NAME/KEY: allele
;  LOCATION: 1559
;  OTHER INFORMATION: 10-509-284  : polymorphic base C or T
;  NAME/KEY: allele
;  LOCATION: 1570
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; OTHER INFORMATION: 10-509-295 : deletion of C
; NAME/KEY: allele
; LOCATION: 1827
; OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
; NAME/KEY: allele
; LOCATION: 2048
; OTHER INFORMATION: 10-511-62 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2323
; OTHER INFORMATION: 10-511-337 : insertion of T
; NAME/KEY: allele
; LOCATION: 2341
; OTHER INFORMATION: 10-512-36 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 2623
; OTHER INFORMATION: 10-512-318 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2832
; OTHER INFORMATION: 10-513-250 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2844
; OTHER INFORMATION: 10-513-262 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 2934
; OTHER INFORMATION: 10-513-352 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 2947
; OTHER INFORMATION: 10-513-365 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 3802
; OTHER INFORMATION: 12-206-81 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 4062
; OTHER INFORMATION: 10-343-231 : deletion of C
; NAME/KEY: allele
; LOCATION: 4088
; OTHER INFORMATION: 12-206-366 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4109
; OTHER INFORMATION: 10-343-278 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 4170
; OTHER INFORMATION: 10-343-339 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 5903
; OTHER INFORMATION: 10-346-23 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6019
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6141
; OTHER INFORMATION: 10-346-263 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6183
; OTHER INFORMATION: 10-346-305 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 6338
; OTHER INFORMATION: 10-347-74 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6375
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 6429
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 6467
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6484
; OTHER INFORMATION: 10-347-220 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 6534
; OTHER INFORMATION: 10-347-271 : polymorphic base A or T
; NAME/KEY: allele
; LOCATION: 6611
; OTHER INFORMATION: 10-347-348 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 7668
; OTHER INFORMATION: 10-348-391 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 8608
; OTHER INFORMATION: 10-349-47 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 8658
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 8703
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 8777
; OTHER INFORMATION: 10-349-216 : deletion of CTG
; NAME/KEY: allele
; LOCATION: 8785
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 8926
; OTHER INFORMATION: 10-349-368 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12171
; OTHER INFORMATION: 10-350-72 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12429
; OTHER INFORMATION: 10-350-332 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 13341
; OTHER INFORMATION: 10-507-170 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 13492
; OTHER INFORMATION: 10-507-321 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 13524
; OTHER INFORMATION: 10-507-353 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 13535

Query Match 2.1%; Score 48.2; DB 4; Length 20674;
Best Local Similarity 45.9%; Pred. No. 0.069;
Matches 240; Conservative 0; Mismatches 278; Indels 5; Gaps 2;

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Qy      1608 AGACATGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCTCAAGATAG 1667
             | |  | |||  |  || ||||  |  |  |||  |  |  || |||       |
Db     11084 ATATTTTAATATTTTTAATTTAATAAATTTTAATTTAATATTAAAATTAAAATTTTAATT 11143

Qy      1668 TAATCCTCCACAGCTAACTGACCTTGATTTCTTTATTCCGAATAACAATAAATATCAATC 1727
             ||||  |  |     |  | |  || |  |   || |   |||   ||||||| | |||
Db     11144 TAATATTAAATTAAAATTTTAATTTTAAATAAATAATTAAAATTTAAATAAATTTAAATT 11203

Qy      1728 TCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAA 1787
             |   |||  || | | |   |   | |   || | ||  || | ||  ||| ||   |
Db     11204 TAAAATTTAAATTTAATTTTAAATAAACATTTAAATTTTTAATTTTAATATTAAATTAAT 11263

Qy      1788 AAAAGAAGTTATACCTGTAACTCA---TAATTTAACATTGAGAAAAACGGTGACTGGTTT 1844
               ||     |||   | |||||  |   |||||||| ||| |   ||    | | |  ||
Db     11264 TTAATTTAATATTAATTTAACTTAATTTAATTTAATATTAATTTAA--CTTAATTTAATT 11321

Qy      1845 AGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAAATAATAAGCAAGA 1904
             |  |    |  || ||||  ||   ||||| || || |||   ||  ||||       |
Db     11322 AATTTAATATTAAATTAAATTTTAATATTTTTAATTTTAATATTAATTTAATTTAATTTA 11381

Qy      1905 ATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAACCTCGAATTTAAAGATGGTAAAGC 1964
             |||   |  | |     ||||     ||   |    | || |  |||||     |
Db     11382 ATTTAATATTAATTAATTTAATTTTAATTTTAATTGCTTCAATATTAAATTAAATTTTAA 11441

Qy      1965 AACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTTATTC 2024
               |  ||| ||||| |       ||| ||| |   |  ||          ||  |||
Db     11442 TATTTTTATTTTAATATTAAATTAAAATTTTAATTTAAAATTAAATATTTAATATTAAAT 11501
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Qy       2025 TTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGCCAAGAAGT 2084
              | |  |       |  |  | ||| | |  ||||        |  ||||||   || ||
Db      11502 TAATTTAAATTTAATATTAAATTTTAATAGCTAAGGAAAATATTTTAATATTAAAAAAAG 11561

Qy       2085 AGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAG 2127
              | ||    ||    |    |    ||||| | || | || |||
Db      11562 ACCATGGCCTTTTTTCAATAGCTAAGGAAAAGCAGGAGAAGAG 11604
```

RESULT 7
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (28257)..(28258)
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; NAME/KEY: misc_feature
; LOCATION: (84773)..(84773)
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; NAME/KEY: misc_feature
; LOCATION: (84808)..(84808)
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; NAME/KEY: misc_feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
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; NAME/KEY: misc_feature
; LOCATION: (148948)..(148948)
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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (319226)..(319226)
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature

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;   LOCATION: (1084830)..(1084830)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1096846)..(1096846)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1119881)..(1119881)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1130881)..(1130881)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1310988)..(1310988)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1313224)..(1313224)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1349473)..(1349473)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1349491)..(1349491)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1470091)..(1470091)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1569020)..(1569020)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1602912)..(1602912)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1603734)..(1603734)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1637998)..(1637998)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (1664854)..(1664855)
;   OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

  Query Match             2.1%;  Score 47.4;  DB 4;  Length 1664976;
  Best Local Similarity   46.3%;  Pred. No. 0.42;
  Matches  156;  Conservative    0;  Mismatches  181;  Indels    0;  Gaps    0;

Qy       1778 TGGAAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAACGGTGA 1837
             | ||  |  | || |||  | ||  | |||| | || |||  |  |   ||||  | |
Db     201070 TTGATAAATATAAGGAATATTTAGGTCTAACTGAAAAATTAGAAGAGCTTAAAAATATTA 201129

Qy       1838 CTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAAATAATA 1897
               | |     ||  || |    |||    | | | | | | |||  |  || | |||| |
Db     201130 AAGATGGGCTTGAAGAGATTTATAATATATGCAACTCTAAGATTTTAGCAATAGATAACA 201189

Qy       1898 AGCAAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAACCTCGAATTTAAAGATG 1957
               |      |  |  | ||   | ||     |  | |   |||| | || ||  ||| |
Db     201190 TTAAGAGGAAGTATAATAAAGAAGATATTGAAATTTACCTAAACAACAAAATTTTAGAGG 201249

Qy       1958 GTAAAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTACCAGAAG 2017
                |||      ||||||   | | | |    ||  |      || |      ||  || |
Db     201250 TTAATAAGGAAATTAATGATATAGAAGAAAGAATATCCTACATTAACCAAAAACTTGATG 201309

Qy       2018 GTTATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTAATAGCC 2077
                    |||  ||   |||||    |      |    |      | ||  ||| || | |
Db     201310 AAATAAACTACAATGAAGAAGAACATAAAAAAATAAAAGAGCTCTATGAAAATAAGAGAC 201369

Qy       2078 AAGAAGTAGCAAATGCTACAGTTTCAAAAACAGGAAT 2114
              ||||| | |  || |  | ||    |||||||| |||
Db     201370 AAGAACTTGATAACGTAAGAGAACAAAAAACAGAAAT 201406


RESULT 8
US-09-601-198-156/c
; Sequence 156, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
;  APPLICANT: Cassell, Gail H.
;  APPLICANT:  Chen, Ellson Y.
;  APPLICANT:  Glass, Jennifer S.
;  APPLICANT:  Glass, John I.
;  APPLICANT:  Heiner, Cheryl R.
;  APPLICANT:  Lefkowitz, Elliot
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
;  TITLE OF INVENTION:  UREALYTICUM
;  FILE REFERENCE: UAB-13452/22
;  CURRENT APPLICATION NUMBER: US/09/601,198
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: 60/073,189
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
;   LENGTH: 1785
;   TYPE: DNA
;   ORGANISM: Ureaplasma urealyticum
US-09-601-198-156

  Query Match             2.1%;  Score 47;  DB 4;  Length 1785;
  Best Local Similarity   46.5%;  Pred. No. 0.062;
  Matches  152;  Conservative    0;  Mismatches  175;  Indels    0;  Gaps    0;

Qy       1613 TGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCTCAAGATAGTAATC 1672
              | || |||  |  |     | ||| |  |    ||  ||     | | | | |  | |||
Db        476 TCAAAGATGATGTTGAGCAAATTGTTCCATATATTAAAGCCGTTGGTTATGGTTTTTATC 417

Qy       1673 CTCCACAGCTAACTGACCTTGATTTCTTTATTCCGAATAACAATAAATATCAATCTCTTA 1732
              | | | |   |  ||          | | |    | ||| || ||  | ||||||  |
Db        416 CCCAAGAAGAATTTGGTGAATTAATGTATTGATCTAATTACTATTTAAATCAATTACCAG 357

Qy       1733 TTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAAAG 1792
               ||    ||| |   ||  |||| |  || || |   ||||  |    ||  ||||  |
Db        356 ATGTTTTTCAATATTATAAAGAAAAGATAATTAAACCTATTATTGATCAAATTAAATCAA 297

Qy       1793 AAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTTAGCTGGTG 1852
              ||  |    | | ||   ||  || || |||   | ||      | |  |  |  |  |
Db        296 AAAGTGATTCAGCAAACGATGTTTCAAAATTAGAAGAACTTTATAATTTTAAATATCATT 237

Qy       1853 ACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAAATAATAAGCAAGAATTGCTTT 1912
              |||  | ||   ||   | |||| |     ||  | | |||  | |  |  |     |
Db        236 ACACTAATATCTATGAACCTTTTAATCAAAAAAGAGATAATTTTTATTATTATTCTGACT 177

Qy       1913 CTCAAACTGTTAAAACAGATAAAACAA 1939
              | |||| | | | | || | ||| ||
Db        176 ATAAAACAGATGATAAAGGTGAAAAAA 150


RESULT 9
US-09-601-198-61/c
; Sequence 61, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
;  APPLICANT: Cassell, Gail H.
;  APPLICANT:  Chen, Ellson Y.
;  APPLICANT:  Glass, Jennifer S.
;  APPLICANT:  Glass, John I.
;  APPLICANT:  Heiner, Cheryl R.
;  APPLICANT:  Lefkowitz, Elliot
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
;  TITLE OF INVENTION:  UREALYTICUM
;  FILE REFERENCE: UAB-13452/22
;  CURRENT APPLICATION NUMBER: US/09/601,198
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: 60/073,189
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 181
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
;   LENGTH: 2418
;   TYPE: DNA
;   ORGANISM: Ureaplasma urealyticum
US-09-601-198-61

  Query Match             2.1%;  Score 47;  DB 4;  Length 2418;
  Best Local Similarity   43.5%;  Pred. No. 0.068;
  Matches  276;  Conservative    0;  Mismatches  350;  Indels    9;  Gaps    1;

Qy       1565 CTGAATTAGATAAGGATAAACTAAAAGACTATCATGGTTTTGGAGACATGAATGATAGTA 1624
Db        638 CTAAAATTACTAATGTTAATAATCAACCAATCGTTAATGTTAATGATTTAGATAGAAAAG 579

Qy       1625 CTTTAGCAGTTGCTAAAATCCTTGTAGAATACGCTCAAGATAGTAATCCTCCACAGCTAA 1684
Db        578 ATAGATTATTAGAAAAAGTCGATGTAAATAAATTACAACAATTAAATACATACACCTATG 519

Qy       1685 CTGACCTTGATTTCTTTATTCCGAATAACAATAAATATCAATCTCTTATTGGAACTCAGT 1744
Db        518 ATGATTTAGGAAATTTAATTATTGACATTAATGATAATTTAAATAAAATAACAACTCAAG 459

Qy       1745 GGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAAAGAAGTTATACCTG 1804
Db        458 ATGCTGTTGCTCATTTTATTGATGAAAATAATAAAGATTATTTTGTTCCTACTAAAGTTG 399

Qy       1805 TAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTTAGCTGGTGACAGAACTAAAG 1864
Db        398 ATTTAAATAAGAATAAAATAAGTATTAACACAAAAGATTTAGATGCAAACCACCACTATC 339

Qy       1865 ATTTCCATTTTGAAATTGAATTAAAAAATAATAAGCAAGAATTGCTTTCTCAAACTGTTA 1924
Db        338 AATTGTTAAATATTGTTGATAAAAACAAGCATGAGCAAATTTTATTAAATTCAAACGAAA 279

Qy       1925 AAACAGATAAAACAAACCTCGAATTTAAAGATGGTAAAGCAACCATTAATTTAAAACATG 1984
Db        278 TTAATCCTTTAAACAGAATTAGCATTATTAAACCACTTGCAATTATTAAACAAGATGCAA 219

Qy       1985 GGGAAAGTTTAACACTTCAAGGTTTACCAGAAGGTTATTCTTACCTTGTCAAAGAAACAG 2044
Db        218 ATAAAAATTTAAACCTACTAACTTTTGATAAGAATTTGTTTAATCGTTCATTAGATGCAA 159

Qy       2045 ATTCTGAAGGCTATAAGGTTAAAGTTAATAGCCAAGAAGTAGCAAATGCTACAGTTTC-- 2102
Db        158 CTTTTATTGATGAAAATCAAAAAGAATATCATGTTAAAGCAAAAACTATTATTGATTCAT 99

Qy       2103 -------AAAAACAGGAATAACAAGTGATGAGACACTTGCTTTTGAAAATAATAAAGAGC 2155
Db          98 TAGGTCAAACACGATTTATAACTAGTGATGAGGTTTTACCTAACCATCATAAATATCAAC 39

Qy       2156 CTGTTGTTCCTACAGGAGTTGATCAAAAGATCAAT 2190
Db          38 TAATTGCTCTTAAATATGATGGTCAAAAAAGTAAT 4


RESULT 10
US-09-627-122-21/c
; Sequence 21, Application US/09627122
; Patent No. 6472521
; GENERAL INFORMATION:
;  APPLICANT:  Uhlmann, Eugen
;  APPLICANT:  Greiner, Beate
;  APPLICANT:  Unger, Eberhard
;  APPLICANT:  Gothe, Gislinde
;  APPLICANT:  Schwerdel, Marc
;  TITLE OF INVENTION:  OLIGONUCLEOTIDES FOR THE INHIBITION OF HUMAN eg5
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE:  02481.1678
;  CURRENT APPLICATION NUMBER: US/09/627,122
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS:  23
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 5340
;   TYPE: DNA
;   ORGANISM: Plasmodium falciparum
US-09-627-122-21

  Query Match             2.1%;  Score 46.8;  DB 4;  Length 5340;
  Best Local Similarity   44.8%;  Pred. No. 0.097;
  Matches  180;  Conservative    0;  Mismatches  222;  Indels    0;  Gaps    0;

Qy       1414 GATACCGATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTACAGG 1473
Db       1124 GACACGAATTATGATAATAATAAAAATGATGATAATAATAAAAATAATCATGATAATAAT 1065

Qy       1474 GAAAAAGGACAAGCTATTGAGTATAGTGGTCTAACTGAGACACAATTGCGTGCGGCTACT 1533
Db       1064 AAAAATAATCATGATAATAATAAAAATAATCATGATAATAATAAAAATGGTGACAATAAT 1005

Qy       1534 CAGTTAGCAATATATTATTTCACTGATAGTGCTGAATTAGATAAGGATAAACTAAAAGAC 1593
Db       1004 AAAAATGATCATGACAATAATAAAAATGGTGACAATAATAATTATGATGATAATAAAATG 945

Qy       1594 TATCATGGTTTTGGAGACATGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAGAA 1653
Db        944 GATCAAGGTCATGATCATAATAATTATCTTTATAATGATGATAATAAAATGGATCAAGGT 885

Qy       1654 TACGCTCAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTTATTCCGAATAAC 1713
Db        884 CATGATCATAATAATTATCTTTATAATGATGATAATAAAATGGATCAAGGTCATGATCAT 825

Qy       1714 AATAAATATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTATT 1773
Db        824 AATAATTATCTTTATAATGATGATAATAAAATGGATCAAGGTGATCATCATAATTATTAT 765

Qy       1774 CGTATGGAAGATAAAAAAGAAGTTATACCTGTAACTCATAAT 1815
Db        764 CTTTATAATGATGATAATAAAATAGATCAAGGTGATCATCAT 723


RESULT 11
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
;  APPLICANT: Bult et al.
;  TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methano
; Patent No. 6503729
;  TITLE OF INVENTION:  jannaschii
;  FILE REFERENCE: PB275
;  CURRENT APPLICATION NUMBER: US/08/916,421B
;  CURRENT FILING DATE:  1997-08-22
;  PRIOR APPLICATION NUMBER: US 60/024,428
;  PRIOR FILING DATE: 1996-08-22
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1664976
;   TYPE: DNA
;   ORGANISM: Methanococcus jannaschii
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (28222)..(28222)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (28257)..(28258)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (84773)..(84773)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (84808)..(84808)
;   OTHER INFORMATION: n equals a, t, c, or g
;   NAME/KEY: misc_feature
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; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
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; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match 2.1%; Score 46.8; DB 4; Length 1664976;

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  Best Local Similarity   45.8%;  Pred. No. 0.58;
  Matches  162;  Conservative    0;  Mismatches  192;  Indels    0;  Gaps    0;

Qy       1871 ATTTTGAAATTGAATTAAAAAATAATAAGCAAGAATTGCTTTCTCAAACTGTTAAAACAG 1930
              | | ||| |    ||| |  |||| ||   ||   || || | |  |     |||
Db     281149 ACTATGATAAATTATTCACTAATAGTATATAAATCTTCCTATTTTTAGAATATAATTATA 281090

Qy       1931 ATAAAACAAACCTCGAATTTAAAGATGGTAAAGCAACCATTAATTTAAAACATGGGGAAA 1990
              || |||||    ||  ||   |   ||    |   |  | || || | | ||| |
Db     281089 TTAGAACAACGTGTAAAAATAGGAAAATTATTAAATTGAGAAGTTAAATATAGGGGTAGG 281030

Qy       1991 GTTTAACACTTCAAGGTTTACCAGAAGGTTATTCTTACCTTGTCAAAGAAACAGATTCTG 2050
              |||  |  | ||    || |  | ||| |  ||       |   |       ||  |
Db     281029 CAATAAAATCTAAAACAATAACTTAGGGTGAAACTATGAAATTTGGATGGGTTAATGTTA 280970

Qy       2051 AAGGCTATAAGGTTAAAGTTAATAGCCAAGAAGTAGCAAATGCTACAGTTTCAAAAACAG 2110
              ||  ||||    |||  || |   |   |||| |||  ||   ||  |||  ||
Db     280969 TTGGAGATAACTGGGAAGAGAAAAAGAAGATAGTAACAACAGCATTAGAGTCATCAATCC 280910

Qy       2111 GAATAACAAGTGATGAGACACTTGCTTTTGAAAATAATAAAGAGCCTGTTGTTCCTACAG 2170
              | ||     || |||  ||   | | ||||||| | |||||| | ||    |  || ||
Db     280909 CAGTAGTTGTTGCTGAACCAGAAGATATTGAAAAAATTAAAGAACTTGGAAATATTAAAG 280850

Qy       2171 GAGTTGATCAAAAGATCAATGGCTATCTAGCTTTGATAGTTATCGCTGGTATCA 2224
                |    ||    |  | |   || | | |||  ||  ||    ||  | ||
Db     280849 TTGCCTCCCATTCCTTAGACGCGGATATTGTTTTAGTAAATAAAAATGACAACA 280796


RESULT 12
US-09-417-485D-5
; Sequence 5, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
;  APPLICANT: Long, David M.
;  APPLICANT:  Metz, Anneke M.
;  APPLICANT:  Love, Ruschelle A.
;  TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
;  FILE REFERENCE: 47714-5009-US
;  CURRENT APPLICATION NUMBER: US/09/417,485D
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 10640
;   TYPE: DNA
;   ORGANISM: Plasmodium falciparum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (834)..(7385)
;   OTHER INFORMATION: TERT gene
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1821)..(1837)
;   OTHER INFORMATION: m at position 1821 = a or c; w at position 1837 =
;   OTHER INFORMATION: a or t.  Xaa (amino acid) at position 330 = Leu or
;   OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

  Query Match             2.0%;  Score 46.6;  DB 4;  Length 10640;
  Best Local Similarity   47.4%;  Pred. No. 0.13;
  Matches  139;  Conservative    0;  Mismatches  154;  Indels    0;  Gaps    0;

Qy       1683 AACTGACCTTGATTTCTTTATTCCGAATAACAATAAATATCAATCTCTTATTGGAACTCA 1742
              ||| || |      |   ||    | |||| |||||||  || |   | | || ||
Db         20 AACCGAACAAATAATAAGTAAGAAGGATAAGAATAAATTACATTTAATAAATGAAATAAT 79

Qy       1743 GTGGCATCCAGAAGATTTAGTTGATATTATTCGTATGGAAGATAAAAAAGAAGTTATACC 1802
                 || ||  |  |||    || | |  |  | |  || ||     ||||  | |
Db         80 AATAGATACATCATTTTTTAAAGAGAATTATGATTTTCAATATTTTTTAGAAAATGTTTT 139

Qy       1803 TGTAACTCATAATTTAACATTGAGAAAAACGGTGACTGGTTTAGCTGGTGACAGAACTAA 1862
                ||    | |||||   || | |||   ||  | |   |||  || |||      ||
Db        140 ATTATTAGAAGATTTAGTTTTAAAAAAGTTGGATAATAAATTAAATGATGAGGATTTTAT 199

Qy       1863 AGATTTCCATTTTGAAATTGAATTAAAAAATAATAAGCAAGAATTGCTTTCTCAAACTGT 1922
              |  |    |  | |||  | ||  | |||||||  | ||||||    |  ||| | |
Db        200 ATTTAAAGAAAATAAAAAAGTATCTATAAATAATTGGAAAGAATGTTATAGTCATATTAA 259

Qy       1923 TAAAACAGATAAAACAAACCTCGAATTTAAAGATGGTAAAGCAACCATTAATT 1975
                |||| |   || |  ||         | || |  ||||   |   | |||||
Db        260 GAAAAAATTAAATATCAAAGGTATGGATGAAAAAAGTAAGATATATAATAATT 312


RESULT 13
US-08-973-462-2
; Sequence 2, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
;  APPLICANT: DRUILHE, PIERRE
;  APPLICANT: DAUBERSIES, PIERRE
;  TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
;  FILE REFERENCE: 0660-0125-0 PCT
;  CURRENT APPLICATION NUMBER: US/08/973,462B
;  CURRENT FILING DATE: 1998-02-06
;  EARLIER APPLICATION NUMBER: PCT/FR96/00894
;  EARLIER FILING DATE: 1996-06-12
;  EARLIER APPLICATION NUMBER: FR 95/07007
;  EARLIER FILING DATE: 1995-06-13
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5361
;   TYPE: DNA
;   ORGANISM: P. falciparum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(5361)
US-08-973-462-2

  Query Match             2.0%;  Score 46.4;  DB 3;  Length 5361;
  Best Local Similarity   40.9%;  Pred. No. 0.12;
  Matches  435;  Conservative    0;  Mismatches  626;  Indels    3;  Gaps    1;

Qy       1115 TTATTGATGGAAAACAGATTGAAAATCCCAATAAAGAGATAGTAGAGCCTTACTCAGTAG 1174
              | | ||| | | ||     |  ||      |||  || | | || |    |    |  ||
Db       3749 TAAATGAAGTAGAAGCAGATTTAATAAAAGATATGGAAAAATTAAAAGAATTAGAAAAAG 3808

Qy       1175 AAGCATATAATGATTTTGAAGAATTTAGCGTTTTAACTACACAAAACTATGCAAAATTTT 1234
              |  ||   | |||| | ||||| | |  | |  ||      | |  |  | |||| ||
Db       3809 CATTATCAGAAGATTCTAAAGAAATAATAGATGCAAAAGATGATACATTAGAAAAAGTTA 3868

Qy       1235 ATTATGCAAAAAATAAAAATGGAAGTTCACAGGTTGTCTATTGCTTTAATGCAGATCTAA 1294
              | | |   || || | |  .   |   |   || ||     |           |||| |
Db       3869 TTGAAGAGGAACATGATATAACGACGACGTTGGATGAAGTTGTAGAATTAAAAGATGTCG 3928

Qy       1295 AATCTCCACCAGACTCTGAAGATGGTGGGAAAACAATGACTCCAGACTTTACAACAGGAG 1354
              ||           |    |||    ||    || |     |  |||   || |  |  ||
Db       3929 AAGAAGACAAGATCGAAAAAGTATCTGATTTAAAAGATCTTGAAGAAGATATATTAAAAG 3988

Qy       1355 AAGTAAAATACACTCATATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGAG 1414
              |||||||| | |    |       |   ||||  | ||  || || |    ||  || | |
Db       3989 AAGTAAAAGAAATCAAAGAACTTGAAAGTGAAATTTTAGAAGATTATAAAGAATTAAAAA 4048

Qy       1415 ATACCGATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTACAGGG 1474
              ||  ||  | || | |||   | |  | |   ||| || ||  ||  |   | | |
Db       4049 CTATTGAAACAGATATTTTAGAAGAGAAAAAAGAAATAGAAAAAGATCATTTTGAAAAAT 4108

Qy       1475 AAAAAGGACAAGCTATTGAGTATAGTGGTCTAACTGAGACACAATTGCGTGCGGCTACTC 1534
                ||| | |||||   ||    |  | |||    |       |||    | |   ||
Db       4109 TCGAAGAAGAAGCTGAAGAAATAAAAGATCTTGAAGCAGATATATTAAAAGAAGTATCTT 4168

Qy       1535 AGTTAGCAATATATTATTTCACTGATAGTGCTGAATTAGATAAGGATAAACTAAAAGACT 1594
              |||| | |  |  |    |   |    |  ||| || | |    |||  | | |
Db       4169 CATTAGAAGTTGAAGAAGAAAAAAAATTAGAAGAAGTACACGAATTAAAAGAAGAGGTAG 4228

Qy       1595 ATCATGGTTT---TGGAGACATGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAG 1651
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Db       4229 AACATATAATAAGTGGTGATGCGCATATAAAAGGTTTGGAAGAAGATGATTTAGAAGAAG 4288

Qy       1652 AATACGCTCAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTTATTCCGAATA 1711

Db       4289 TAGATGATTTAAAAGGAAGTATATTAGACATGTTAAAGGGAGATATGGAATTAGGGGATA 4348

Qy       1712 ACAATAAATATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTA 1771

Db       4349 TGGATAAGGAAAGTTTAGAAGATGTAACAACAAAACTTGGAGAAAGAGTTGAATCCTTAA 4408

Qy       1772 TTCGTATGGAAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAAAA 1831

Db       4409 AAGATGTTTTATCTAGTGCATTAGGCATGGATGAAGAACAAATGAAAACAAGAAAAAAAG 4468

Qy       1832 CGGTGACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAA 1891

Db       4469 CTCAAAGACCTAAGTTGGAAGAAGTATTATTAAAAGAAGAGGTTAAAGAAGAACCAAAGA 4528

Qy       1892 ATAATAAGCAAGAATTGCTTTCTCAAACTGTTAAAACAGATAAAACAAACCTCGAATTTA 1951

Db       4529 AAAAAATAACAAAAAAGAAAGTAAGGTTTGATATTAAGGATAAGGAACCAAAAGATGAAA 4588

Qy       1952 AAGATGGTAAAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTAC 2011

Db       4589 TAGTAGAAGTTGAAATGAAAGATGAAGATATAGAAGAAGATGTAGAAGAAGATATAGAAG 4648

Qy       2012 CAGAAGGTTATTCTTACCTTGTCAAAGAAACAGATTCTGAAGGCTATAAGGTTAAAGTTA 2071

Db       4649 AAGATATAGAAGAAGATAAAGTTGAAGATATAGATGAAGATATAGATGAAGATATAGGTG 4708

Qy       2072 ATAGCCAAGAAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACAC 2131

Db       4709 AAGACAAAGATGAAGTTATAGATTTAATAGTCCAAAAAGAGAAACGCATTGAAAAGGTTA 4768

Qy       2132 TTGCTTTTGAAAATAATAAAGAGCCTGTTGTTCCTACAGGAGTT 2175

Db       4769 AAGCGAAAAAGAAAAAATTAGAAAAAAAAGTTGAAGAAGGTGTT 4812


RESULT 14
US-08-973-462-1
; Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
;  APPLICANT: DRUILHE, PIERRE
;  APPLICANT: DAUBERSIES, PIERRE
;  TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
;  FILE REFERENCE: 0660-0125-0 PCT
;  CURRENT APPLICATION NUMBER: US/08/973,462B
;  CURRENT FILING DATE: 1998-02-06
;  EARLIER APPLICATION NUMBER: PCT/FR96/00894
;  EARLIER FILING DATE: 1996-06-12
;  EARLIER APPLICATION NUMBER: FR 95/07007
;  EARLIER FILING DATE: 1995-06-13
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 6152
;   TYPE: DNA
;   ORGANISM: P. falciparum
US-08-973-462-1

  Query Match             2.0%;  Score 46.4;  DB 3;  Length 6152;
  Best Local Similarity   40.9%;  Pred. No. 0.13;
  Matches  435;  Conservative    0;  Mismatches  626;  Indels    3;  Gaps    1;

Qy       1115 TTATTGATGGAAAACAGATTGAAAATCCCAATAAAGAGATAGTAGAGCCTTACTCAGTAG 1174

Db       3993 TAAATGAAGTAGAAGCAGATTTAATAAAAGATATGGAAAAATTAAAAGAATTAGAAAAAG 4052

Qy       1175 AAGCATATAATGATTTTGAAGAATTTAGCGTTTTAACTACACAAAACTATGCAAAATTTT 1234

Db       4053 CATTATCAGAAGATTCTAAAGAAATAATAGATGCAAAAGATGATACATTAGAAAAAGTTA 4112

Qy       1235 ATTATGCAAAAAATAAAAATGGAAGTTCACAGGTTGTCTATTGCTTTAATGCAGATCTAA 1294

Db       4113 TTGAAGAGGAACATGATATAACGACGACGTTGGATGAAGTTGTAGAATTAAAAGATGTCG 4172

Qy       1295 AATCTCCACCAGACTCTGAAGATGGTGGGAAAACAATGACTCCAGACTTTACAACAGGAG 1354

Db       4173 AAGAAGACAAGATCGAAAAAGTATCTGATTTAAAAGATCTTGAAGAAGATATATTAAAAG 4232

Qy       1355 AAGTAAAATACACTCATATTGCAGGTCGTGACCTCTTTAAATATACTGTGAAACCAAGAG 1414

Db       4233 AAGTAAAAGAAATCAAAGAACTTGAAAGTGAAATTTTAGAAGATTATAAAGAATTAAAAA 4292

Qy       1415 ATACCGATCCTGACACTTTCTTAAAACATATCAAAAAAGTAATTGAGAAGGGTTACAGGG 1474

Db       4293 CTATTGAAACAGATATTTTAGAAGAGAAAAAAGAAATAGAAAAAGATCATTTTGAAAAAT 4352

Qy       1475 AAAAAGGACAAGCTATTGAGTATAGTGGTCTAACTGAGACACAATTGCGTGCGGCTACTC 1534

Db       4353 TCGAAGAAGAAGCTGAAGAAATAAAAGATCTTGAAGCAGATATATTAAAAGAAGTATCTT 4412

Qy       1535 AGTTAGCAATATATTATTTCACTGATAGTGCTGAATTAGATAAGGATAAACTAAAAGACT 1594

Db       4413 CATTAGAAGTTGAAGAAGAAAAAAAATTAGAAGAAGTACACGAATTAAAAGAAGAGGTAG 4472

Qy       1595 ATCATGGTTT---TGGAGACATGAATGATAGTACTTTAGCAGTTGCTAAAATCCTTGTAG 1651

Db       4473 AACATATAATAAGTGGTGATGCGCATATAAAAGGTTTGGAAGAAGATGATTTAGAAGAAG 4532

Qy       1652 AATACGCTCAAGATAGTAATCCTCCACAGCTAACTGACCTTGATTTCTTTATTCCGAATA 1711

Db       4533 TAGATGATTTAAAAGGAAGTATATTAGACATGTTAAAGGGAGATATGGAATTAGGGGATA 4592

Qy       1712 ACAATAAATATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATATTA 1771

Db       4593 TGGATAAGGAAAGTTTAGAAGATGTAACAACAAAACTTGGAGAAAGAGTTGAATCCTTAA 4652

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Db       4653 AAGATGTTTTATCTAGTGCATTAGGCATGGATGAAGAACAAATGAAAACAAGAAAAAAAG 4712

Qy       1832 CGGTGACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAAAA 1891

Db       4713 CTCAAAGACCTAAGTTGGAAGAAGTATTATTAAAAGAAGAGGTTAAAGAAGAACCAAAGA 4772

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Qy       1952 AAGATGGTAAAGCAACCATTAATTTAAAACATGGGGAAAGTTTAACACTTCAAGGTTTAC 2011

Db       4833 TAGTAGAAGTTGAAATGAAAGATGAAGATATAGAAGAAGATGTAGAAGAAGATATAGAAG 4892

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Qy       2072 ATAGCCAAGAAGTAGCAAATGCTACAGTTTCAAAAACAGGAATAACAAGTGATGAGACAC 2131

Db       4953 AAGACAAAGATGAAGTTATAGATTTAATAGTCCAAAAAGAGAAACGCATTGAAAAGGTTA 5012

Qy       2132 TTGCTTTTGAAAATAATAAAGAGCCTGTTGTTCCTACAGGAGTT 2175

Db       5013 AAGCGAAAAAGAAAAAATTAGAAAAAAAAGTTGAAGAAGGTGTT 5056


RESULT 15
US-09-491-785-1
; Sequence 1, Application US/09491785
; Patent No. 6316211
; GENERAL INFORMATION:
;  APPLICANT: Zalacain, Magdalena
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;  APPLICANT: Biswas, Sanjoy
;  APPLICANT: Burnham, Martin K. R.
;  APPLICANT: Van Horn, Stephanie
;  TITLE OF INVENTION: thdF
;  FILE REFERENCE: GM10249
;  CURRENT APPLICATION NUMBER: US/09/491,785
;  CURRENT FILING DATE: 2000-01-26
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-09-491-785-1

  Query Match             2.0%;  Score 45.4;  DB 4;  Length 1380;
  Best Local Similarity   51.2%;  Pred. No. 0.14;
  Matches  106;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy       1710 TAACAATAAATATCAATCTCTTATTGGAACTCAGTGGCATCCAGAAGATTTAGTTGATAT 1769
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Db        975 TAAAAATGAAGATGTAATCGTAATTGTTAATAAAATGGATTTAGAGCAAAACATAGATAT 1034

Qy       1770 TATTCGTATGGAAGATAAAAAAGAAGTTATACCTGTAACTCATAATTTAACATTGAGAAA 1829
              || |    |  ||||||  | ||  | ||  ||  ||| ||| | || ||  || | | |
Db       1035 TAATGAAGTTAAAGATATGATAGGTGATACGCCATTAATTCAAACTTCAATGTTAAAACA 1094

Qy       1830 AACGGTGACTGGTTTAGCTGGTGACAGAACTAAAGATTTCCATTTTGAAATTGAATTAAA 1889
              |   |  | || |  |   |       || |  ||||||    ||||     ||| || |
Db       1095 AGAAGGTATTGATGAATTAGAAATACAAATTCGAGATTTGTTCTTTGGTGGAGAAGTACA 1154

Qy       1890 AAATAATAAGCAAGAATTGCTTTCTCA 1916
              |||| |  |       |   ||||| |
Db       1155 AAATCAAGATATGACTTATGTTTCTAA 1181


Search completed: August 19, 2003, 13:18:42
Job time : 164 secs
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